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<120> ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR

<130> 3492-WO

<140> --to be assigned--

<141> 2004-11-04

<150> 60/518,166

<151> 2003-11-07

<160> 77

<170> PatentIn version 3.2

<210> 1

<211> 2475

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)..(2475)

<400> 1

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ctg	ctg	cag	gtg	gca	agc	tct	ggg	aac	atg	aag	gtc	ttg	cag	gag	ccc	96
Leu	Leu	Gln	Val	Ala	Ser	Ser	Gly	Asn	Met	Lys	Val	Leu	Gln	Glu	Pro	
			20					25					30			

acc	tgc	gtc	tcc	gac	tac	atg	agc	atc	tct	act	tgc	gag	tgg	aag	atg	144
Thr	Cys	Val	Ser	Asp	Tyr	Met	Ser	Ile	Ser	Thr	Cys	Glu	Trp	Lys	Met	
		35					40					45				

aat	ggt	ccc	acc	aat	tgc	agc	acc	gag	ctc	cgc	ctg	ttg	tac	cag	ctg	192
Asn	Gly	Pro	Thr	Asn	Cys	Ser	Thr	Glu	Leu	Arg	Leu	Leu	Tyr	Gln	Leu	
	50					55					60					

gtt	ttt	ctg	ctc	tcc	gaa	gcc	cac	acg	tgt	atc	cct	gag	aac	aac	gga	240
Val	Phe	Leu	Leu	Ser	Glu	Ala	His	Thr	Cys	Ile	Pro	Glu	Asn	Asn	Gly	
65					70					75				80		

ggc	gcg	ggg	tgc	gtg	tgc	cac	ctg	ctc	atg	gat	gac	gtg	gtc	agt	gcg	288
Gly	Ala	Gly	Cys	Val	Cys	His	Leu	Leu	Met	Asp	Asp	Val	Val	Ser	Ala	
			85						90					95		

gat	aac	tat	aca	ctg	gac	ctg	tgg	gct	ggg	cag	cag	ctg	ctg	tgg	aag	336
Asp	Asn	Tyr	Thr	Leu	Asp	Leu	Trp	Ala	Gly	Gln	Gln	Leu	Leu	Trp	Lys	
			100					105					110			

ggc tcc ttc aag ccc agc gag cat gtg aaa ccc agg gcc cca gga aac Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn 115 120 125	384
ctg aca gtt cac acc aat gtc tcc gac act ctg ctg ctg acc tgg agc Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser 130 135 140	432
aac ccg tat ccc cct gac aat tac ctg tat aat cat ctc acc tat gca Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala 145 150 155 160	480
gtc aac att tgg agt gaa aac gac ccg gca gat ttc aga atc tat aac Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn 165 170 175	528
gtg acc tac cta gaa ccc tcc ctc cgc atc gca gcc agc acc ctg aag Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys 180 185 190	576
tct ggg att tcc tac agg gca cgg gtg agg gcc tgg gct cag tgc tat Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr 195 200 205	624
aac acc acc tgg agt gag tgg agc ccc agc acc aag tgg cac aac tcc Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser 210 215 220	672
tac agg gag ccc ttc gag cag cac ctc ctg ctg ggc gtc agc gtt tcc Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser 225 230 235 240	720
tgc att gtc atc ctg gcc gtc tgc ctg ttg tgc tat gtc agc atc acc Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr 245 250 255	768
aag att aag aaa gaa tgg tgg gat cag att ccc aac cca gcc cgc agc Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser 260 265 270	816
cgc ctc gtg gct ata ata atc cag gat gct cag ggg tca cag tgg gag Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu 275 280 285	864
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tgt ctt acc aag ctc ttg ccc tgt ttt ctg gag cac aac atg aaa agg Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg 305 310 315 320	960
gat gaa gat cct cac aag gct gcc aaa gag atg cct ttc cag ggc tct Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser 325 330 335	1008
gga aaa tca gca tgg tgc cca gtg gag atc agc aag aca gtc ctc tgg Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp 340 345 350	1056

cca gag agc atc agc gtg gtg cga tgt gtg gag ttg ttt gag gcc ccg	1104
Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro	
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Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe	
370 375 380	
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Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu	
385 390 395 400	
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Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly	
405 410 415	
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Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu	
420 425 430	
ctt cca cct tcg gga agt acg agt gct cac atg ccc tgg gat gag ttc	1344
Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe	
435 440 445	
cca agt gca ggg ccc aag gag gca cct ccc tgg ggc aag gag cag cct	1392
Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro	
450 455 460	
ctc cac ctg gag cca agt cct cct gcc agc ccg acc cag agt cca gac	1440
Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp	
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Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala	
485 490 495	
tac cgc agc ttc agc aac tcc ctg agc cag tca ccg tgt ccc aga gag	1536
Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu	
500 505 510	
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Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro	
515 520 525	
gag atg ccc tgt gtc ccc cag ctc tct gag cca acc act gtg ccc caa	1632
Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln	
530 535 540	
cct gag cca gaa acc tgg gag cag atc ctc cgc cga aat gtc ctc cag	1680
Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln	
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cat ggg gca gct gca gcc ccc gtc tcg gcc ccc acc agt ggc tat cag	1728
His Gly Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln	
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Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val	
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Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser	
595 600 605	
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Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala	
610 615 620	
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Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly	
625 630 635 640	
tgc cct ggg gac cct gcc cca gtc cct gtc ccc ttg ttc acc ttt gga	1968
Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly	
645 650 655	
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Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser	
660 665 670	
agc tcc cca gag cac ctg ggt ctg gag ccg ggg gaa aag gta gag gac	2064
Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp	
675 680 685	
atg cca aag ccc cca ctt ccc cag gag cag gcc aca gac ccc ctt gtg	2112
Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val	
690 695 700	
gac agc ctg ggc agt ggc att gtc tac tca gcc ctt acc tgc cac ctg	2160
Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu	
705 710 715 720	
tgc ggc cac ctg aaa cag tgt cat ggc cag gag gat ggt ggc cag acc	2208
Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr	
725 730 735	
cct gtc atg gcc agt cct tgc tgt ggc tgc tgc tgt gga gac agg tcc	2256
Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser	
740 745 750	
tgc ccc cct aca acc ccc ctg agg gcc cca gac ccc tct cca ggt ggg	2304
Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly	
755 760 765	
gtt cca ctg gag gcc agt ctg tgt ccg gcc tcc ctg gca ccc tgc ggc	2352
Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly	
770 775 780	
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Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly	
785 790 795 800	
aat gct cag agc tca agc cag acc ccc aaa atc gtg aac ttt gtc tcc	2448
Asn Ala Gln Ser Ser Ser Gln Thr Pro Lys Ile Val Asn Phe Val Ser	
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 <213> Homo sapien

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Thr Cys Val Ser Asp Tyr Met Ser Ile Ser Thr Cys Glu Trp Lys Met
 35 40 45

Asn Gly Pro Thr Asn Cys Ser Thr Glu Leu Arg Leu Leu Tyr Gln Leu
 50 55 60

Val Phe Leu Leu Ser Glu Ala His Thr Cys Ile Pro Glu Asn Asn Gly
 65 70 75 80

Gly Ala Gly Cys Val Cys His Leu Leu Met Asp Asp Val Val Ser Ala
 85 90 95

Asp Asn Tyr Thr Leu Asp Leu Trp Ala Gly Gln Gln Leu Leu Trp Lys
 100 105 110

Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg Ala Pro Gly Asn
 115 120 125

Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu Leu Thr Trp Ser
 130 135 140

Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His Leu Thr Tyr Ala
 145 150 155 160

Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe Arg Ile Tyr Asn
 165 170 175

Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala Ser Thr Leu Lys
 180 185 190

Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp Ala Gln Cys Tyr
 195 200 205

Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys Trp His Asn Ser
 210 215 220

Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly Val Ser Val Ser
 225 230 235 240

Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr Val Ser Ile Thr
 245 250 255

Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn Pro Ala Arg Ser
 260 265 270

Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly Ser Gln Trp Glu
 275 280 285

Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro His Trp Lys Asn
 290 295 300

Cys Leu Thr Lys Leu Leu Pro Cys Phe Leu Glu His Asn Met Lys Arg
 305 310 315 320

Asp Glu Asp Pro His Lys Ala Ala Lys Glu Met Pro Phe Gln Gly Ser
 325 330 335

Gly Lys Ser Ala Trp Cys Pro Val Glu Ile Ser Lys Thr Val Leu Trp
 340 345 350

Pro Glu Ser Ile Ser Val Val Arg Cys Val Glu Leu Phe Glu Ala Pro
 355 360 365

Val Glu Cys Glu Glu Glu Glu Glu Val Glu Glu Glu Lys Gly Ser Phe
 370 375 380

Cys Ala Ser Pro Glu Ser Ser Arg Asp Asp Phe Gln Glu Gly Arg Glu
 385 390 395 400

Gly Ile Val Ala Arg Leu Thr Glu Ser Leu Phe Leu Asp Leu Leu Gly
 405 410 415

Glu Glu Asn Gly Gly Phe Cys Gln Gln Asp Met Gly Glu Ser Cys Leu
 420 425 430

Leu Pro Pro Ser Gly Ser Thr Ser Ala His Met Pro Trp Asp Glu Phe
 435 440 445

Pro Ser Ala Gly Pro Lys Glu Ala Pro Pro Trp Gly Lys Glu Gln Pro
 450 455 460

Leu His Leu Glu Pro Ser Pro Pro Ala Ser Pro Thr Gln Ser Pro Asp
 465 470 475 480

Asn Leu Thr Cys Thr Glu Thr Pro Leu Val Ile Ala Gly Asn Pro Ala
 485 490 495

Tyr Arg Ser Phe Ser Asn Ser Leu Ser Gln Ser Pro Cys Pro Arg Glu
 500 505 510

Leu Gly Pro Asp Pro Leu Leu Ala Arg His Leu Glu Glu Val Glu Pro
 515 520 525

Glu Met Pro Cys Val Pro Gln Leu Ser Glu Pro Thr Thr Val Pro Gln
 530 535 540

Pro Glu Pro Glu Thr Trp Glu Gln Ile Leu Arg Arg Asn Val Leu Gln
 545 550 555 560

His Gly Ala Ala Ala Ala Pro Val Ser Ala Pro Thr Ser Gly Tyr Gln
 565 570 575

Glu Phe Val His Ala Val Glu Gln Gly Gly Thr Gln Ala Ser Ala Val
 580 585 590

Val Gly Leu Gly Pro Pro Gly Glu Ala Gly Tyr Lys Ala Phe Ser Ser
 595 600 605

Leu Leu Ala Ser Ser Ala Val Ser Pro Glu Lys Cys Gly Phe Gly Ala
 610 615 620

Ser Ser Gly Glu Glu Gly Tyr Lys Pro Phe Gln Asp Leu Ile Pro Gly
 625 630 635 640

Cys Pro Gly Asp Pro Ala Pro Val Pro Val Pro Leu Phe Thr Phe Gly
 645 650 655

Leu Asp Arg Glu Pro Pro Arg Ser Pro Gln Ser Ser His Leu Pro Ser
 660 665 670

Ser Ser Pro Glu His Leu Gly Leu Glu Pro Gly Glu Lys Val Glu Asp
 675 680 685

Met Pro Lys Pro Pro Leu Pro Gln Glu Gln Ala Thr Asp Pro Leu Val
 690 695 700

Asp Ser Leu Gly Ser Gly Ile Val Tyr Ser Ala Leu Thr Cys His Leu
 705 710 715 720

Cys Gly His Leu Lys Gln Cys His Gly Gln Glu Asp Gly Gly Gln Thr
 725 730 735

Pro Val Met Ala Ser Pro Cys Cys Gly Cys Cys Cys Gly Asp Arg Ser
 740 745 750

Ser Pro Pro Thr Thr Pro Leu Arg Ala Pro Asp Pro Ser Pro Gly Gly
 755 760 765

Val Pro Leu Glu Ala Ser Leu Cys Pro Ala Ser Leu Ala Pro Ser Gly
 770 775 780

Ile Ser Glu Lys Ser Lys Ser Ser Ser Ser Phe His Pro Ala Pro Gly
 785 790 795 800

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Val Gly Pro Thr Tyr Met Arg Val Ser
 820 825

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 <212> DNA
 <213> Artificial

<220>
 <223> Light chain variable sequence

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 <222> (1)..(327)

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 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 atc ttt ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
 Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 4
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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

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 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Phe Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc aac agc	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Ser	
20 25 30	
tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	
atc tat ggt gca tcc agc agg gcc cct ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser	
50 55 60	
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65 70 75 80	
cct gaa gat ttt gca gtg tat tac tgt cag cag tat gat cac tca gca	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala	
85 90 95	
ggg tgg acg ttc ggc caa ggg acc aag gtg gag atc aaa	327
Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

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<213> Artificial

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<223> Synthetic Construct

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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Pro Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp His Ser Ala
.85 90 95

Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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gaa aga gcc acc ctc tcc tgc agg gcc agt cag act gtt aac agc gac 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Asn Ser Asp
20 25 30
tac tta gcc tgg tac cag cag aaa ccg ggc cag gct ccc agg ctc ctc 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc agt 192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
cct gaa gat ttt gca gtc tat tac tgt cag cag tat ggt agg tca cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
85 90 95
ccg tgg acg ttc ggc caa ggg acc aaa gtg gat atc aaa 327
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
100 105

<210> 8
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<212> PRT
<213> Artificial

<220>

<223> Synthetic Construct

<400> 8

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 1 5 10 15

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 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 9

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<212> DNA

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<223> Light chain variable sequence

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<222> (1)..(327)

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gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt agc agc gac 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp
 20 25 30

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

atc tat ggt gca tct agc agg gcc tct ggc atc cca gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

ggc agt ggg ttt ggg aca gac ttc act ctc acc atc agc aga ctg gag 240
 Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

cct gaa gat ttt gca ata tat tac tgt cag cag tat ggt agc tca cct 288
 Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
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ccg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa 327
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Ser Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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<223> Light chain variable sequence

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1 5 10 15	

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt aac agc aac	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn	
20 25 30	

tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc	144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

atc tat ggt aca tcc tac agg gcc act ggc atc cca gac agg ttc agt	192
Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	
50 55 60	

ggc agt ggg tct ggg aca gac ttc act ctc acc atc acc aga ctg gag	240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu	
65 70 75 80	

cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca cca	288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro	
85 90 95	

ccg tgg acg ttc ggc caa ggg aca cga ctg gag att aaa	327
Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys	
100 105	

<210> 12

<211> 109

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 12

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Ser Asn
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Thr Ser Tyr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 13
 <211> 327
 <212> DNA
 <213> Artificial

<220>
 <223> Light chain variable sequence

<220>
 <221> CDS
 <222> (1)..(327)

<400> 13
 gat att gtg ctg acg cag act cca gcc acc ctg tct ttg tct cca ggg 48
 Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt ggc agc agc 96
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 20 25 30
 tac tta gcc tgg tac cag cag aga cct ggc cag gct ccc agg ctc ctc 144
 Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 atc tat ggt gca tcc agc agg gcc act ggc atc ccg gac agg ttc agt 192
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 ggc agt ggg tct ggg aca gac ttc act ctc acg atc agc aga ctg gag 240
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 cct gaa gat ttt gca gtg tat tat tgt cag cag tat gga agt tca cct 288
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 ccg tgg atg ttc ggc caa ggg acc aag gtg gag atc aaa 327
 Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 14
 <211> 109

<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 14

Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Pro Trp Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 15
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 15

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 16
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
115

<210> 17
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 17
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 18
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 18

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 19
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1) .. (345)

<400> 19
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 20
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 20

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 21
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 21
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 22
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 22

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 23
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 23
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 24
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 24

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 25
 <211> 345
 <212> DNA
 <213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 25

gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg	48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

<210> 26

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 26

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 27
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 27
 gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 28
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 28

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 29
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 29

gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 30

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 30

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 31
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 31
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tcc tca
Val Ser Ser
115

345

<210> 32
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 32

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 33
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1) .. (345)

<400> 33
 gag gtt cag ttg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 34
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 34

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 35

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 35

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tcc tca 345
Val Ser Ser
115

<210> 36
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 36

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 37
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 37

gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

48

tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac atg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 38
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 38

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 39
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 39
gag gtt cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg 48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca ggc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg agt gcc gag gac atg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tac ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 40
<211> 115

<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 40

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Ser Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 41
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 41

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Arg Gly Arg Tyr Tyr Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 43
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 43
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 44
 <211> 115
 <212> PRT
 <213> Artificial

<220>

<223> Synthetic Construct

<400> 44

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 45

<211> 345

<212> DNA

<213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 45

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tac ttc acc cac tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 46
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Arg Tyr Tyr Phe Thr His Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
115

<210> 47
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 47
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80
caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
aga ggg agg tac tgg tac aac aac tgg ggc cag gga acc ctg gtc acc 336
Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
gtc tcc tca 345
Val Ser Ser
115

<210> 48
<211> 115
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Asn Asn Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 49
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 49

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

```

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag      192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
  50                      55                      60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
  65                      70                      75                      80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca      288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                      90                      95

aga ggg agg tac tac ttc acg agg tgg ggc cag gga acc ctg gtc acc      336
Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
                100                      105                      110

gtc tcc tca
Val Ser Ser
    115

```

```

<210> 50
<211> 115
<212> PRT
<213> Artificial

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```

<220>
<223> Synthetic Construct

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<400> 50

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```

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1                      5                      10                      15

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
                20                      25                      30

```

```

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                35                      40                      45

```

```

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50                      55                      60

```

```

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65                      70                      75                      80

```

```

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                      90                      95

```

```

Arg Gly Arg Tyr Tyr Phe Thr Arg Trp Gly Gln Gly Thr Leu Val Thr
                100                      105                      110

```

```

Val Ser Ser
    115

```

<210> 51
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 51
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 52
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 52

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 53
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 53
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 54
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 54

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 55
 <211> 345

<212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 55
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 gtc tcc tca 345
 Val Ser Ser
 115

<210> 56
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 56
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 57
<211> 345
<212> DNA
<213> Artificial

<220>
<223> Heavy chain variable sequence

<220>
<221> CDS
<222> (1)..(345)

<400> 57
gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30
gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60
ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

aga ggg agg tac tgg ttc ccg tgg tgg ggc cag gga acc ctg gtc acc 336
 Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

gtc tcc tca 345
 Val Ser Ser
 115

<210> 58
 <211> 115
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 58

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Phe Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 59
 <211> 345
 <212> DNA
 <213> Artificial

<220>

<223> Heavy chain variable sequence

<220>

<221> CDS

<222> (1)..(345)

<400> 59

gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn	
20 25 30	

gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta	144
Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

tca ggt att ggt act ggt ggt gcc aca agc tat gca gac tcc gtg aag	192
Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys	
50 55 60	

ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt	240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu	
65 70 75 80	

caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca	288
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
85 90 95	

aga ggg agg tac tgg tac ccg tgg tgg ggc cag gga acc ctg gtc acc	336
Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr	
100 105 110	

gtc tcc tca	345
Val Ser Ser	
115	

<210> 60

<211> 115

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 60

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
20 25 30

Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Thr Gly Gly Ala Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Gly Arg Tyr Trp Tyr Pro Trp Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 61
 <211> 345
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain variable sequence

<220>
 <221> CDS
 <222> (1)..(345)

<400> 61
 gag gtt cag ttg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt aga aat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Asn
 20 25 30
 gct atg ttc tgg gtt cgc cag gct cca gga aaa ggt ctg gag tgg gta 144
 Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 tca ggt att ggt act ggt ggt gcc aca aac tat gca gac tcc gtg aag 192
 Ser Gly Ile Gly Thr Gly Gly Ala Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 ggc cga ttc acc atc tcc aga gac aat gcc aag aac tcc ttg tat ctt 240
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 65 70 75 80
 caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt gca 288
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 64
 <211> 116
 <212> PRT
 <213> Artificial

<220>
 <223> 27A1 heavy chain variable region

<400> 64

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Ala Ile Ile Trp Phe Glu Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Glu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Lys Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 65
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> 5A1 light chain variable region

<400> 65

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr His Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 66
 <211> 123
 <212> PRT
 <213> Artificial

<220>
 <223> 5A1 heavy chain variable region

<400> 66

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Thr Cys Ala Gly Ser Gly Phe Thr Phe Ser Asn Phe
 20 25 30

Val Met His Trp Val Arg Gln Thr Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Ser Leu Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Asp Arg Pro Met Val Arg Gly Val Ile Ile Asp Tyr Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 67
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> 63 light chain variable region

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Thr Trp
 20 25 30

Leu Ala Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 68
 <211> 117
 <212> PRT
 <213> Artificial

<220>
 <223> 63 heavy chain variable region

<400> 68

Glu Val Gln Val Leu Glu Ser Gly Gly Asn Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Phe Tyr Cys
 85 90 95

Ala Lys Asp Asn Arg Gly Phe Phe His Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 69
 <211> 107
 <212> PRT
 <213> Artificial

<220>
 <223> 1B7 light chain variable region

<400> 69

Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Arg
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ile Ala Ser Ile Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 70
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Primers

<220>
 <221> misc_feature
 <222> (21)..(21)
 <223> N is A or G

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> N is G or T

<400> 70
 gtcgacgccg ccaccatgga nttngggctg agctgg

36

<210> 71
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Primers

<400> 71
 cttgaccagg cagcccaggg c

21

<210> 72
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 72
atcaaacgta cggtggctgc accatctgtc ttcac

36

<210> 73
<211> 49
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 73
gtttaaacgc ggccgcggat cctaacactc tcccctgttg aagctcttt

49

<210> 74
<211> 99
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 74
gtcgacgccg ccacatgga aaccccagcg cagcttctct tcctcctgct actctggctc
ccagataccg ctagcgaaat tgtgttgacg cagtctcca

60

99

<210> 75
<211> 99
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 75
tggagactgc gtcaacacaa tttcgctagc ggtatctggg agccagagta gcaggaggaa
gagaagctgc gctgggggtt ccatggtggc ggcgtcgac

60

99

<210> 76
<211> 57
<212> DNA
<213> Artificial

<220>
<223> Primers

<400> 76

atgggggtcaa cgcctatcct tggcctcctc ctggctgttc tccaaggagt cgctagc

57

<210> 77

<211> 327

<212> PRT

<213> Homo sapiens

<400> 77

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325